



Figure 1

Sequence Name:

GW.S.ctgl6335-000003.31.0

Figure 1A SEQ ID NO:01

LLAPTGSLFRNCTQDGWSETFPRPNLACGVNVNDSSNEKRSYLLKLKVMYTVGYSSSLVM
LLVALGILCAFRRLHCTRNYIHMHLFVSFILRALSNFIKDAVLFSSDDVTYCDHRGCKL
VMVLFXYCIMANYSWLLVEGSTFTHxLAISFFSERKYLGQFVAFGWGSPAIFVALWAIAR
HFLEDVGCWDINANASIWWIIRGPVILSILNFILFINILRILMRKLRTQETRGNEVSHYK
RLARSTLLLIPLFGIHYIVFAFSPEDAMEIQLFF

Figure 1B SEQ ID NO:02

CTCTTGGCACCCACAGGTTTCCTTGTTCCGAAACTGCACACAGGATGGCTGGTCAGAAACC
TTCCCCAGGCCTAATCTGGCCTGTGGCGTTAATGTGAACGACTCTTCCAACGAGAAGCGG
CACTCCTACCTGCTGAAGCTGAAAGTCATGTACACCGTGGGCTACAGCTCCTCCCTGGTC
ATGCTCCTGGTCGCCCTTGGCATCCTCTGTGCTTTCCGGAGGCTCCACTGCACTCGCAAC
TACATCCACATGCACCTGTTCTGTGCTTTCATCCTTCGTGCCCTGTCCAACCTCATCAAG
GACGCCGTGCTCTTCTCCTCAGATGATGTACCTACTGCGATGCCCACAGGGCGGGCTGC
AAGCTGGTCATGGTGCTGTTC

Figure 1C SEQ ID NO:03

TACTGCATCATGGCCAACTACTCCTGGCTGCTGGTGGAAGGCTCTACCTTCACACATNTC
CTCGCCATCTCCTTCTTCTCTGAAAGAAAGTACCTCCAGGGATTTGTGGCATTTCGGATGG
GGTTCTCCAGCCATTTTTGTTGCTTTGTGGGCTATTGCCAGACACTTTCTGGAAGATGTT
GGGTGCTGGGACATCAATGCCAACGCATCCATCTGGTGGATCATTTCGTGGTCCTGTGATC
CTCTCCATCCTGATTAATTTTCATCCTTTTCATAAACATTCTAAGAATCCTGATGAGAAAA
CTTAGAACCCAAGAAACAAGAGGAAATGAAGTCAGCCATTATAAGCGCCTGGCCAGGTCC
ACTCTCCTGCTGATCCCCCTCTTTGGCATCCACTACATCGTCTTCGCCTTCTCCCCAGAG
GACGCTATGGAGATCCAGCTGTTTTTT

Figure 1D SEQ ID NO:04

CTCTTGGCACCCACAGGTTTCCTTGTTCCGAAACTGCACACAGGATGGCTGGTCAGAAACC
TTCCCCAGGCCTAATCTGGCCTGTGGCGTTAATGTGAACGACTCTTCCAACGAGAAGCGG
CACTCCTACCTGCTGAAGCTGAAAGTCATGTACACCGTGGGCTACAGCTCCTCCCTGGTC
ATGCTCCTGGTCGCCCTTGGCATCCTCTGTGCTTTCCGGAGGCTCCACTGCACTCGCAAC
TACATCCACATGCACCTGTTCTGTGCTTTCATCCTTCGTGCCCTGTCCAACCTCATCAAG
GACGCCGTGCTCTTCTCCTCAGATGATGTACCTACTGCGATGCCCACAGGGCGGGCTGC
AAGCTGGTCATGGTGCTGTTC
TACTGCATCATGGCCAACTACTCCTGGCTGCTGGTGGAAGGCTCTACCTTCACACATNTC
CTCGCCATCTCCTTCTTCTCTGAAAGAAAGTACCTCCAGGGATTTGTGGCATTTCGGATGG
GGTTCTCCAGCCATTTTTGTTGCTTTGTGGGCTATTGCCAGACACTTTCTGGAAGATGTT
GGGTGCTGGGACATCAATGCCAACGCATCCATCTGGTGGATCATTTCGTGGTCCTGTGATC
CTCTCCATCCTGATTAATTTTCATCCTTTTCATAAACATTCTAAGAATCCTGATGAGAAAA
CTTAGAACCCAAGAAACAAGAGGAAATGAAGTCAGCCATTATAAGCGCCTGGCCAGGTCC
ACTCTCCTGCTGATCCCCCTCTTTGGCATCCACTACATCGTCTTCGCCTTCTCCCCAGAG
GACGCTATGGAGATCCAGCTGTTTTTT



Figure 2

Sequence Name:

GW.S.ctg16490-000000.17.0

Figure 2A SEQ ID NO:05

PTFILFSFQPGDKRTRKHICVYWEGSEGGHWSTEGCSHVHNSNGSYTKCKCFHLSSFAVLVA
LAPKDPVLTVITQVGLTISLLCLFLAILTFLLCRPIQNTSTSLHLELSLCLFLAHLFLT
GINRTEPELCSIIAGLLHFLYLACFTWMLLEGLHLFLTVRNLKVANYTSTGRFKKRFMYF
VGYGIPAVIIAIVSAIVGPQNYGTFTHCWLKLDKGFIWSFMGPVAVIILNLVFFYFQVLWIL
RSKLSSLNKEVSTIQDTRVMTFKAISQLFILGCSWGLGFFMVEEVGKTIGSIIAYSFTII
NTLQGVLLFVVHCLLNRRQVR

Figure 2B SEQ ID NO:06

CCCACTTTCATACTATTCTCTTTCCAGCCTGGTGACAAGAGAACAAAACATATCTGTGTC
TACTGGGAGGGATCAGAGGGAGGCCACTGGTCCACGGAGGGCTGCTCTCATGTGCACAGC
AACGGTTCTTACACCAAATGCAAGTGCTTCCATCTGTCCAGCTTTGCCGTCCTCGTGGCT
CTTGCCCCCAAGGAGGACCCTGTGCTGACCGTGATCACCCAGGTGGGGCTGACCATCTCT
CTGCTGTGCCTCTTCCCTGGCCATCCTCACCTTCCCTCCTGTGCCGCCCATCCAGAACACC
AGCACCTCCCTCCATCTAGAGCTCTCCCTCTGCCTCTTCCCTGGCCCACCTCCTGTTCCCTG
ACGGGCATCAACAGAACTGAGCCTGAGGTGCTGTGCTCCATCATTGCAGGGCTGCTGCAC
TTCCTCTACCTGGCTTGCTTACCTGGATGCTCCTGGAAGGGCTGCACCTCTTCCCTCACC
GTCAGGAACCTCAAGGTGGCCAACTACACCAGCACGGGCAGATTCAAGAAGAGGTTTCATG
TACCCTGTAGGCTACGGGATCCCAGCTGTGATTATTGCTGTGTGTCAGCAATAGTTGGACCC
CAGAATTATGGAACATTTACTCACTGTTGGCTCAAGCTTGATAAAGGATTCATCTGGAGC
TTCATGGGGCCAGTAGCAGTCATTATCTTGATAAACCTGGTGTCTACTTCCAAGTTCTG
TGGATTTTGAGAAGCAAACCTTCCCTCCCTCAATAAAGAAGTTTCCACCATTTCAGGACACC
AGAGTCATGACATTTAAAGCCATTTCTCAGCTATTTATCCTGGGCTGTTCTTGGGGCCTT
GGTTTTTTTATGGTTGAAGAAGTAGGGAAGACGATTGGATCAATCATTGCATACTCATTC
ACCATCATCAACACCCTTCAGGGAGTGTTGCTCTTTGTGGTACACTGTCTCCTTAATCGC
CAGGTAAGG



Figure 3

Sequence Name:

GW.S.ctg13100-000000.33.0

Figure 3A SEQ ID NO:07

QHSDAVHDLDDLVDITWVGILLSLVCLLICIFTFCFFRGLQSDRNTIHKNLCSLFFVAELL
FLIGINRTDQPACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESEHSRRKYFYLVG
YGMPALIVAVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMNVIFLGIALYKMFH
HTAILKPESGCLDNIKLKINIPKSIYIYMYICMCV

Figure 3B SEQ ID NO:08

CAGCACAGTGATGCGGTCCATGACCTCCTTCTGGATGTGATCACGTGGGTGGAATTTTG
CTGTCCCTTGTTTGTCTCCTGATTTGCATCTTCACATTTTGCTTTTCCGGGGGCTCCAG
AGTGACCGTAACACCATCCACAAGAACCCTCTGCATCAGTCTCTTTGTAGCAGAGCTGCTC
TTCCTGATTGGGATCAACCGAAGTACCAACCAATTGCCTGTGCTGTTTTCGCTGCCCTG
TTACATTTCTTCTTCTGGCTGCCTTCACCTGGATGTTCTGGAGGGGGTGCAGCTTTAT
ATCATGCTGGTGGAGGTTTTTGAGAGTGAACATTCACGTAGGAAATACTTTTATCTGGTC
GGCTATGGGATGCCTGCACTCATTGTGGCTGTGTCAGCTGCAGTAGACTACAGGAGTTAT
GGAACAGATAAAGTATGTTGGCTCCGACTTGACACCTACTTCATTTGGAGTTTTATAGGA
CCAGCAACTTTGATAATTATGCTTAATGTAATCTTCCTTGGGATTGCTTTATATAAAATG
TTTCATCATACTGCTATACTGAAACCTGAATCAGGCTGTCTTGATAACATCAAGTTAAAA
ATTAATATTCCAATTATAAAATCTATTTATATCTATATGTATATATGCATGTGTGTG



Figure 4

Sequence Name:

GW.A.ctg12444-000001.0.2

Figure 4A SEQ ID NO:09

GNVAVAFVYYKSIGPLLSSSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEK
ITFTLSHRKTDYRSLCAFWNYSPTMNGSWSSEGCETYSNETHTSCRCNHLTHFAILM
SSGPSIIKDYNILTRITQLGIIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAE
LVFLVGINTNTNKFCSIIAGLLHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYI
FGYLSPAVVVGFSALGYRYYGTTKVCWLSTENNFIWSFIGPACLIILVCIYKIVITIQL
SDDH

Figure 4B SEQ ID NO:10

GGCAATGTTGCAGTTGCATTTGTATATTATAAGAGTATTGGTCCTTTGCTTTCATCATCT
GACAACTTCTTATTGAAACCTCAAATTATGATAATTCTGAAGAGGAGGAAAGAGTCATA
TCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCACATTATATGAACTTGAAAAA
ATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGAGTCTATGTGCATTT
TGGAATTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACA
TACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTTGCAATTTTG
ATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAA
CTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTACCTTCTGGTTCTTC
AGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTGTAGCCTATTTCTT
GCTGAACTTGTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATC
ATTGCCGACTGCTACACTACTTCTTTTAGCTGCTTTTGCATGGATGTGCATTGAAGGC
ATACATCTCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATTTTGCACAAGAAT
TTTTATATCTTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTTCGGCAGCACTAGGA
TACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAACCTTTATTGG
AGTTTTATAGGACCAGCATGCCTAATCATTCTTGTATGTATATATAAAATTGTTATTACA
ATTCAAAAAAGTGATGATCAT



Figure 5

Sequence Name:

GW.S.ctg12789-000004.100.0

Figure 5A SEQ ID NO:11

GAWATTGCSVAALYLDSTACFCNHSTSFAILLQIYEVQGPEEESLLRTLSTFVGC GVSFCA
LTTTFLLFLVAGVPKSERTTVHKNLTFSLASAEGFLMTSEWAKANEACVAVTVAMHFLFL
VAFSWMLVEGLLLWRKVAVSMHPGPGMRLYHATGWGVPVGIVAVTLAMLP HDYVAPGHC
WLVNHTNAIWAFFVGPVLFVLTVS

Figure 5B SEQ ID NO:12

GGTGCCTGGGCCACACAGGCTGCTCCGTGGCTGCCCTGTACCTGGACTCCACCGCCTGC
TTCTGCAACCACAGCACCAGCTTTGCCATCCTGCTGCAAATCTATGAAGTACAGAGAGGC
CCTGAGGAGGAGTCGCTGCTGAGGACTCTGTCAATTTGTGGGCTGTGGCGTGTCTTCTGC
GCCCTCACCACCACCTTCTTGCTCTTCCCTGGTGGCCGGGGTCCCCAAGTCAGAGCGAACC
ACAGTCCACAAGAACCTCACCTTCTCCCTGGCCTCTGCCGAGGGCTTCCTCATGACCAGC
GAGTGGGCCAAGGCCAATGAGGTGGCATGTGTGGCTGTCACAGTCGCAATGCACTTCCTC
TTTCTGGTGGCATTCTCCTGGATGCTGGTGGAGGGGCTGCTGCTGTGGAGGAAGGTGGTA
GCTGTGAGCATGCACCCGGGCCAGGCATGCGGCTCTACCACGCCACAGGCTGGGGCGTG
CCTGTGGGCATCGTGGCGGTCAACCCTGGCCATGCTCCCCCATGACTACGTGGCCCCCGGA
CATTGCTGGCTCAATGTGCACACAAATGCCATCTGGGCCTTCGTGGGGCCTGTGCTCTTC
GTGCTGACTGTGAGC



Figure 6

Sequence Name:

GW.A.ctg12776-000000.33.0

Figure 6A SEQ ID NO:13

MKSPRRTTLCLMFIVYSSKAALNWNYESITHPLLHEHEPAGEEALRQKRAVATKSPTAE
EYTVNIEISFENASFLDPIKAYLNSLSFPIHGNNTDQITDILSINVTTVCRPAGNEIWCS
CETGYGWPRERCLHNLICQERDVFLPGHHCSCLKELPPNGPFCLLQEDVTLNMRVRLNVG
FQEDLMNTSSALYRSYKTDLETARKGYGILPGFKGVTVTGFKSGSVVVTYEVKTTPPSLE
LIHKANEQVVQSLNQTYKMDYNSFQAVTINESNFFVTPEIIFEGDTVSLVCEKEVLSSNV
SWRYEEQQLEIQNSSRFSIYALFNNMTSVSKLTIHNITPGDAGEYVCKLILDI FEYECK
KKIDVMPIQILANEEMKVMCDNNFVSLNCCSQGNVNWSKVEWKQEGKINIPGTPETDIDS
SCSRYTLKADGTQCPSGSGTTVIYTCEFISAYGARGSANIKVTFISVANLTITPDPI SV
SEGQNFISIKCISDVSNYDEVYWNWSAGIKIYQRFYTRRYLDGAESVLT VKTSTREWNGT
YHCIFRYKNSYSIATKDVIHPLPLKLNIMVDPLEATVSCSGSHHIKCCIEEDGDYKVF
HTGSSSLPAAKEVNKKQVCYKHNFNASSVSWCSKTVDVCCHFTNAANNVSWSPMKLNLV
PGENITCQDPVIGVGEKQVQKLCRFSNVSSPESPIGGTITYKCVGSQWEEKRND CIS
APINSLQMAKLIKSPSQDEMLPTYLKDLSISIDKAEHEISSPSGLGAIINILDLLSTV
PTQVNSEMMTVLSTVNVILGKPV LNTWKVLQQQWNTNQSQLLHSVERFSQALQSGDSPPL
SFSQTNVQMSSMVIKSSHPEYQQRFVFPYFDLWGNVVIDKSYLENLQSDSSI VTMAFP
LQAILAQDIQENNFAESLVMTTTVSHNTTMPFRISMTFKNNSPSGGETKCVFNNFRLANN
TGGWDSSGCVVEEGDGNVTCICDHLTSFSLMSPDSPDPSSLLGILLDIISYVGVGFSI
LSLAACLVVEAVVWKSVTKNRTSYMRHTCIVNIAASLLVANTWFI VVAIQDNRYILCKT
ACVAATFFIHFFYLSVFFWMLTLGLMLFYRLVFI LHETSRSTQKAI AFCLGYGCPLAISV
ITLGATQPREVYTRKNVVCNLN WEDTKALLAFAPALII VVNVITITIVVITKILRPSIGD
KPCKQEKSSLFQISKSIGVLTPLLGLTWGFGLTTFVPGTNLVFHIIFAILNVFQLFILLF
GCLWDLKQEALLNKFSLSRWSSQHSKTSLSGSSTPVFSMSSPISRRFNNLFGKTGTYNVST
PEATSSSLENSSSASSLLN

Figure 6B SEQ ID NO:14

ATGAAATCCCCAAGGAGAACCACCTTTGTGCCTCATGTTTATTGTGATTTATTCTTCCAAA
GCTGCACTGAAGTGAATTACGAGTCTACTATTATCATCCTTTGAGTCTTCATGAACATGAA
CCAGCTGGTGAAGAGGCACTGAGGCAAAAACGAGCCGTTGCCACAAAAAGTCCTACGGCT
GAAGAATACACTGTTAATATTGAGATCAGTTTTGAAAATGCATCCTTCCTGGATCCTATC
AAAGCCTACTTGAACAGCCTCAGTTTTCCAATTTCATGGGAATAACACTGACCAAATTACC
GACATTTTGAGCATAAATGTGACAACAGTCTGCAGACCTGCTGGAAATGAAATCTGGTG
TCCTGCGAGACAGGTTATGGGTGGCCTCGGGAAAGGTGTCTTCACAATCTCATTGTGCAA
GAGCGTGACGTCTTCCTCCCAAGGCAACCATTGCAGTTGCCTTAAAGAACTGCCTCCCAAT
GGACCTTTTTGCCTGCTTCAGGAAGATGTTACCTGAACATGAGAGTCAGACTAAATGTA
GGCTTTCAAGAAGACCTCATGAACACTTCTCCGCCCTCTATAGGTCTACAAGACCGAC
TTGGAAACAGCGTCCCGAAGGGTTACGGAATTTTACCAGGCTTCAAGGGCGTGACTGTG
ACAGGGTTCAAGTCTGGAAGTGTGGTTGTGACATATGAAGTCAAGACTACACCACCATCA
CTTGAGTTAATACATAAAGCCAATGAACAAGTTGTACAGAGCCTCAATCAGACCTACAAA
ATGGACTACAACCTCTTCAAGCAGTTACTATCAATGAAAGCAATTTCTTTGTACACCA
GAAATCATCTTTGAAGGGGACACAGTCACTGCTGGTGTGTGAAAAGGAAGTTTGTCTCC
AATGTGTCTTGGCGCTATGAAGAACAGCAGTTGGAAATCCAGAACAGCAGCAGATTCTCG
ATTTACACCGCACTTTTCAACAACATGACTTCGGTGTCCAAGCTCACCATCCACAACATC
ACTCCAGGTGATGCAGGTGAATATGTTTGCAAACCTGATATTAGACATTTTGAATATGAG
TGCAAGAAGAAAATAGATGTTATGCCCATCCAAATTTTGCAAATGAAGAAATGAAGGTG
ATGTGCGACAACAATCCTGTATCTTTGAACTGCTGCAGTCAGGGTAATGTTAATTGGAGC
AAAGTAGAATGGAAGCAGGAAGGAAAAATAAATATTCCAGGAACCCCTGAGACAGACATA
GATTCTAGCTGCAGCAGATACACCCTCAAGGCTGATGGAACCCAGTGCCCAAGCGGGTCTG

FEB 21 2003

TCTGGAACAACAGTCATCTACACTTGTGAGTTCATCAGTGCCTATGGAGCCAGAGGCAGT
GCAAACATAAAAGTGACATTTCATCTCTGTGGCCAATCTAACAATAACCCCGGACCCAATT
TCTGTTTCTGAGGGACAAAACCTTTTCTATAAAATGCATCAGTGATGTGAGTAACTATGAT
GAGGTTTATTGGAACACTTCTGCTGGAATTAATAATATACCAAAGATTTTATACACGAGG
AGGTATCTTGATGGAGCAGAATCAGTACTGACAGTCAAGACCTCGACCAGGGAGTGGAAT
GGAACCTATCACTGCATATTTAGATATAAGAATTCATACAGTATTGCAACCAAAGACGTC
ATTGTTACCCCGCTGCTCTAAAGCTGAACATCATGGTTGATCCTTTGGAAGCTACTGTT
TCATGCAGTGGTTCCCATCACATCAAGTGCTGCATAGAGGAGGATGGAGACTACAAAGTT
ACTTTCCATACGGGTTCCTCATCCCTTCCTGCTGCAAAAAGAAGTTAACAAAAACAAGTG
TGCTACAAACACAATTTCAATGCAAGCTCAGTTTCCTGGTGTTCAAAACTGTTGATGTG
TGTGTCACTTTACCAATGCTGCTAATAATTCAGTCTGGAGCCCATCTATGAAGCTGAAT
CTGGTTCCCTGGGGAAAACATCACATGCCAGGATCCCGTAATAGGTGTGCGAGAGCCGGG
AAAGTCATCCAGAAGCTATGCCGGTTCTCAAACGTTCCAGCAGCCCTGAGAGTCCCAT
GGCGGGACCATCACTTACAAATGTGTAGGCTCCAGTGGGAGGAGAAGAGAAATGACTGC
ATCTCTGCCCCAATAAACCTAGCTGCTCCAGATGGCTAAGGCTTTGATCAAGAGCCCCCTCT
CAGGATGAGATGCTCCCTACATACCTGAAGGATCTTTCTATTAGCATAGACAAAGCGGAA
CATGAAATCAGTCTTCTCCTGGGAGTCTGGGAGCCATTATTAACATCCTTGATCTGCTC
TCAACAGTTCCAACCCAAGTAAATTCAGAAATGATGACGCACGTGCTCTCTACGGTTAAT
GTCATCCTTGGCAAGCCCGTCTTGAACACCTGGAAGGTTTTACAACAGCAATGGACCAAT
CAGAGTTCAAGCTACTACATTAGTGGAAAGATTTTCCAAGCATTACAGTCGGGAGAT
AGCCCTCCTTTGTCCTTCTCCCAAACCTAATGTGCAGATGAGCAGCATGGTAATCAAGTCC
AGCCACCCAGAAACCTATCAACAGAGGTTTGTGTTTCCCATACTTTGACCTCTGGGGCAAT
GTGGTCATTGACAAGAGCTATCTAGAAAACCTTGCAAGTGGATTGCTCTATTGTCACCATG
GCTTTCCCAACTCTCCAAGCCATCCTTGCCAGGATATCCAGGAAAATAACTTTGCAGAG
AGCTTAGTGATGACAACCACTGTGAGCCACAATAACAATATGCCATTACAGGATTTCAATG
ACTTTTAAGAACAATAGCCCTTCAGGCGGGCAACGAAGTGTGTCTTCTGGAACCTCAGG
CTTGCCAACAACACAGGGGGGTGGGACAGCAGTGGGTGCTATGTAGAAGAAGGTGATGGG
GACAATGTCACCTGTATCTGTGACCACCTAACATCATTCTCCATCCTCATGTCCCCTGAC
TCCCCAGATCCTAGTTCTCTCCTGGGAATACTCCTGGATATTATTTCTTATGTTGGGGTG
GGCTTTTCCATCTTGAGCTTGGCAGCCTGTCTAGTTGTGGAAGCTGTGGTGTGGAAATCG
GTGACCAAGAACCGGACTTCTTATATGCGCCACACCTGCATAGTGAATATCGCTGCCTCC
CTTCTGGTCGCAACACCTGGTTTATTGTGGTGTGCTGCCATCCAGGACAATCGCTACATA
CTCTGCAAGACAGCCTGTGTGGCTGCCACCTTCTTCATCCACTTCTTCTACCTCAGCGTC
TTCTTCTGGATGCTGACACTGGGCCTCATGCTGTTCTATCGCCTGGTTTTCTATTCTGCAT
GAAACAAGCAGGTCCACTCAGAAAGCCATTGCCTTCTGTCTTGGCTATGGCTGCCCCACTT
GCCATCTCGGTTCATCACGCTGGGAGCCACCCAGCCCCGGGAAGTCTATACGAGGAAGAAT
GTCTGTTGGCTCAACTGGGAGGACACCAAGGCCCTGCTGGCTTTCGCCATCCCAGCACTG
ATCATTGTGGTGGTGAACATAACCATCACTATTGTGGTTCATCACCAGATCCTGAGGCCT
TCCATTGGAGACAAGCCATGCAAGCAGGAGAAGAGCAGCCTGTTTCAGATCAGCAAGAGC
ATTGGGGTCTCACACCACTCTTGGGCCTCACTTGGGGTTTTGGTCTCACCCTGTGTTT
CCAGGGACCAACCTTGTGTTCCATATCATATTTGCCATCCTCAATGTCTTCCAGGGATTA
TTTCATTGTCGAGATGGTCTTACAGCACTCAAAGTCAACATCCCTGGGTTTCATCCACA
CCTGTGTTTTCTATGAGTTCTCCAATATCAAGGAGATTTAACAATTTGTTTGGTAAAACA
GGAACGTATAATGTTTTCCACCCAGGAAGCAACCAGCTCATCCCTGGAAAACCTCATCCAGT
GCTTCTTCGTTGCTCAAC



Figure 7

Sequence Name:

GW.S.ctg12776-000000.175.0

Figure 7A SEQ ID NO:15

ILNSKSISNWTFI RDRNSSYILLHSVNSFARRLFIDNIPVDISDVFIHTMGTTISGDNIG
KNFTFSMRINDTSNEVTGRVLISRDELRKVPSPSQVISIAFPTIGAILEASLLENVTVNG
LVLSAILPKELKRISLIFEKISKSEERRTQCVGWHSVENRWDQQACKMIQENSQQAVCKC
RPSKLFTSFSILMSPHILESILTYITYVGLGISICSLILCLSIEVLVWSQVTKTEITYL
RHVCIVNIAATLLMADVWFIVASFLSGPITHHKGCVAATFFVHFFYLSVFFWMLAKALLI
LYGIMIVFHTLPKSVLVASLFSVGYGCP LAIAAITVAATEPGKGYLRPEICWLNWDMTKA
LLAFVIPALAI VVVNLITVTLVIVKTQRAAIGNSMFQEVRAIVRISKNI AILTPLLGLTW
GFGVATVIDDRSLAFHII FSLNFAQFFILVFGTILDPKV

Figure 7B SEQ ID NO:16

ATTCTTAACAGCAAAGCATCTCCA ACTGGACTTTCATTTCGTGACAGAAACAGCAGCTAT
ATCCTGCTACATTCAGTCAACTCCTTTGCAAGAAGGCTATTCATAGATAACATCCCTGTT
GACATATCAGATGTCTTCATT CATACTATGGGCACCACCATATCTGGAGATAACATTGGA
AAAAATTTCACTTTTTCTATGAGAATTAATGACACCAGCAATGAAGTCACTGGGAGAGTG
TTGATCAGCAGAGATGA ACTTCGGAAGGTGCCTTCCCCTTCTCAGGTCATCAGCATTGCA
TTTCCA ACTATTGGGGCTATTTTGAAGCCAGTCTTTTGGAAAATGTTACTGTAAATGGG
CTTGTCCTGTCTGCCATTTTGCCCAAGGA ACTTAAAGAATCTCACTGATTTTTGAAAAG
ATCAGCAAGTCAGAGGAGAGGAGGACACAGTGTGTTGGCTGGCACTCTGTGGAGAACAGA
TGGGACCAGCAGGCCTGCAAATGATTCAAGAAA ACTCCCAGCAAGCTGTTTGCAAATGT
AGGCCAAGCAAATTGTTTACCTCTTTCTCAATTCTTATGTCACCTCACATCTTAGAGAGT
CTGATTCTGACTTACATCACATATGTAGGCCTGGGCATTTCTATTTGCAGCCTGATCCTT
TGCTTGTCATTGAGGTCCTAGTCTGGAGCCAAGTGACAAAGACAGAGATCACCTATTTA
CGCCATGTGTGCATTGTTAACATTGCAGCCACTTTGCTGATGGCAGATGTGTGGTTCATT
GTGGCTTCCTTTCTTAGTGGCCCAATAACACACCACAAGGGATGTGTGGCAGCCACATTT
TTTGTTCA TTTCTTTTACCTTTCTGTATTTTTCTGGATGCTTGCCAAGGCACTCCTTATC
CTCTATGGAATCATGATTGTTTTCCATACCTTGCCCAAGTCAGTCCCTGGTGGCATCTCTG
TTTTTCAGTGGGCTATGGATGCCCTTTGGCCATTGCTGCCATCACTGTTGCTGCCACTGAA
CCTGGCAAAGGCTATCTACGACCTGAGATCTGCTGGCTCAACTGGGACATGACCAAAGCC
CTCCTGGCCTTCGTGATCCCAGCTTTGGCCATCGTGGTAGTAAACCTGATCACAGTCACA
CTGGTGATTGTCAAGACCCAGCGAGCTGCCATTGGCAATTCCATGTTCCAGGAAGTGAGA
GCCATTGTGAGAATCAGCAAGAACATCGCCATCCTCACACCACTTCTGGGACTGACCTGG
GGATTTGGAGTAGCCACTGT CATCGATGACAGATCCCTGGCCTTCCACATTATCTTCTCC
CTGCTCAATGCATTCCAGGGTTTCTTCATCCTAGTGT TTGGAACCATCCTGGATCCAAAG
GTA



Figure 8

Sequence Name:

GW.S.ctg16790-000000.13.0

Figure 8A SEQ ID NO:17

GTTGDWSSEGCSTEVRPEGTVCCCDHLTFFALLLPTLDQSTVHILTRISQAGCGVSMIFL
AFTIILYAFLRLSRERFKSEDA PKIHVALGGSFLNLAFLVNVGSGSKGSDAACWARGA
VFHYFLLCAFTWMGLEAFHLYLLAVRVFNTYFGHYFLKLSLVGWGLPALMVI GTGSANSY
GLYTIRDRENRTSLELCWFREGTTMYALYITVHGYFLITFLFGMVVLALVVKIFTLSRA
TAVKERGKNRKKVLTILGLSSLVGVTWGLAIFTPLGLSTVYIFALFNSLQVDFYILIFY

Figure 8B SEQ ID NO:18

GGGACCACTGGAGACTGGTCTTCTGAGGGCTGCTCCACGGAGGTCAGACCTGAGGGGACC
GTGTGCTGCTGTGACCACCTGACCTTTTTCGCCCTGCTCCTGAGACCCACCTTGGACCAG
TCCACGGTG CATATCCTCACACGCATCTCCAGGCGGGCTGTGGGGTCTCCATGATCTTC
CTGGCCTTACCATTATTCTTTATGCCTTTCTGAGGCTTCCCGGGAGAGGTTCAAGTCA
GAAGATGCCCCAAAGATCCACGTGGCCCTGGGTGGCAGCCTGTTCCCTCCTGAATCTGGCC
TTCTTGGTCAATGTGGGGAGTGGCTCAAAGGGGTCTGATGCTGCCTGCTGGGCCCCGGGG
GCTGTCTTCCACTACTTCCTGCTCTGTGCCTTCACCTGGATGGGCCTTGAAGCCTTCCAC
CTCTACCTGCTCGCTGTCAGGGTCTTCAACACCTACTTCGGGCACTACTTCCTGAAGCTG
AGCCTGGTGGGCTGGGGCCTGCCCCCCTGATAGGGAGAACCGCACCTCTCTGGAGCTATGCTGGTTC
TACGGCCTCTACACCATCCGTGATAGGGAGAACCGCACCTCTCTGGAGCTATGCTGGTTC
CGTGAAGGGACAACCATGTACGCCCTCTATATCACCGTCCACGGCTACTTCCTCATCACC
TTCCTCTTTGGCATGGTGGTCTGGCCCTGGTGGTCTGGAAGATCTTACCCTGTCCCGT
GCTACAGCGGTCAAGGAGCGGGGAAGAACCGGAAGAAGGTGCTCACCCTGCTGGGCCTC
TCGAGCCTGGTGGGTGTGACATGGGGGTGGCCATCTTACCCCGTGGGCCTCTCCACC
GTCTACATCTTTGCACTTTTCAACTCCTTGCAAGTTGATTTTTACATATTGATCTTCTAT



Figure 9

Sequence Name:

GW.S.ctg12776-000000.172.0

Figure 9A SEQ ID NO:19

NHILDTA AISNWAFIPKNASSDLLQSVNLFARQLHIHNNSENIVNELFIQTKGFHINHN
TSEKSLNFSMSMNNTTEDILGMVQIPRQELRKLWPNASQAISIAFPTLGAILREHLQNV
SLPRQVNLVLSVVLPERLQEIILTFEKINKTRNARAQCVGWHSKRRWDEKACQMMLDI
RNEVKCRCNYTSVVMFSILMSSKSMDDKVLDYITCIGLSVLSILSLVLCLEATVWSRV
VVTEISYMRHVCIVNIAVSLLTANVWFIIGSHFNKAQDYNMCAVATFFSHFFYLSLFFW
MLFKALLIYIGILVIFRMMKSRMMVIGFAIGYGCPLIIAVTTVAITEPEKGYIRPEACW
LNWDNTKALXAFAPFVIVAVNLIVVLVAVNTQRPSIGSSKSQDVVIMRISKNVAIL
TPLLGLTWGFGIATLIEGTSITFHIIFALLNAFQFFILLFGTIMDHKV

Figure 9B SEQ ID NO:20

AACCACATCCTCGACACAGCAGCCATTTCAAACCTGGGCTTTTCATTCCCAACAAAAATGCC
AGCTCGGATTTGTTGCAGTCAGTGAATTTGTTTGCCAGACAACTCCACATCCACAATAAT
TCTGAGAACATTGTGAATGAACTCTTCATTAGACAAAAGGGTTTCACATCAACCATAAT
ACCTCAGAGAAAAGCCTCAATTTCTCCATGAGCATGAACAATACCACAGAAGATATCTTA
GGAATGGTACAGATTCCCAGGCAAGAGCTAAGGAAGCTGTGGCCAAATGCATCCCAAGCC
ATTAGCATAGCTTTCCCAACCTTGGGGGCTATCCTGAGAGAAGCCCACTTGCAAAATGTG
AGTCTTCCAGACAGGTAAATGGTCTGGTGCTATCAGTGGTTTTACCAGAAAGGTTGCAA
GAAATCATACTACCTTCGAAAAGATCAATAAAACCCGCAATGCCAGAGCCAGTGTGTT
GGCTGGCACTCCAAGAAAAGGAGATGGGATGAGAAAAGCGTGCCAAATGATGTTGGATATC
AGGAACGAAGTGAAATGCCGCTGTAACCTACACCAGTGTGGTGATGTCTTTTCCATTCTC
ATGTCTCCAAATCGATGACCGACAAAGTTCTGGACTACATCACCTGCATTGGGCTCAGC
GTCTCAATCCTAAGCTTGGTTCTTTGCCTGATCATTGAAGCCACAGTGTGGTCCCGGGTG
GTTGTGACGGAGATATCATACATGCGTCACGTGTGCATCGTGAATATAGCAGTGTCCCTT
CTGACTGCCAATGTGTGGTTTATCATAGGCTCTCACTTTAACATTAAGGCCAGGACTAC
AACATGTGTGTGCAGTGACATTTTTCAGCCACTTTTCTACCTCTCTCTGTTTTTCTGG
ATGCTCTTCAAAGCATTGCTCATCATTTATGGAATATTGGTCATTTTCCGTAGGATGATG
AAGTCCCGAATGATGGTCATTGGCTTTGCCATTGGCTATGGGTGCCATTGATCATTGCT
GTCACTACAGTTGCTATCACAGAGCCAGAGAAAGGCTACATAAGACCTGAGGCCTGTTGG
CTTAACCTGGGACAATAACAAAGCCCTTTAAGCATTGTCATCCCGGCGTTTCGTATTGTG
GCTGTAAATCTGATTGTGGTTTTGGTTGTTGCTGTCAACACTCAGAGGCCCTCTATTGGC
AGTTCCAAGTCTCAGGATGTGGTCATAATTATGAGGATCAGCAAAAATGTTGCCATCCTC
ACTCCACTGCTGGGACTGACCTGGGGTTTTGGAATAGCCACTCTCATAGAAGGCACTTCC
TTGACGTTCCATATAATTTTTGCCTTGCTCAATGCTTTCCAGGGTTTTTTCATCCTGCTG
TTTGAACCATATGATCACAAGGTA